

Applicant(s): Bianca A. Thomae et al.
PHENYLETHANOLAMINE-N-METHYLTRANSFERASE
SEQUENCE VARIANTS

Figure 1 – page 1

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CTGGCACTGGGTGGTAACCAGCAAGCCAGCTGGCATCCGCATCCAGGGTTTGTTCATG
1  -----+-----+-----+-----+-----+-----+ 60
GACCGTGACCCACCATTTGGTCGTTTCGGTCGACCGTAGGCGTAGGTCCCAAACAAAGTTAC

ATGTCTCGTGGAGAATATGGAGGGGCTGGTGCCAGGACTGTCCTTGGCTTTGCCTCGGGG
61  -----+-----+-----+-----+-----+-----+ 120
TACAGAGCACCTCTTATACCTCCCCGACCACGGTCCTGACAGGAACCGAAACGGAGCCCC

TGTGAACGGGGTCAGTGACCTCTAAACTAACCTGCCTCTCAGTTCTGAATCCAGACAGA
121 -----+-----+-----+-----+-----+-----+ 180
ACACTTGCCCCAGTCACTGGAGATTTTGATTGGACGGAGAGTCAAGACTTAGGTCTGTCT

ATCAATCCTCAGCTGTGTCTCGCTCCACACCCCCCTGCCCTGGAAGCCAGGGAAGGTTGGA
181 -----+-----+-----+-----+-----+-----+ 240
TAGTTAGGAGTCGACACAGAGCGAGGTGTGGGGGACGGGACCTTCGGTCCCTTCCAACCT

GGTGCTAGGGGGTCAGGCTCCCCCTCTGTGACCCCTGCAGCTGTTGTGGTGACTCATGTCC
241 -----+-----+-----+-----+-----+-----+ 300
CCACGATCCCCCAGTCCGAGGGGAGACACTGGGGACGTCGACAACACCACTGAGTACAGG

CAACCTAGCTGCCTCTCCCAAGGAGACTTTCCCCTGGGACAAGGGGGAGGGAATGGCATG
301 -----+-----+-----+-----+-----+-----+ 360
GTTGGATCGACGGAGAGGGTTCTCTGAAAGGGGACCCTGTTCCCCCTCCCTTACCGTAC

GAGGAGGCCCCACATCAAGCGGGGCCAGGAACCCACGGTGGCAGGAGCTGGGCTGGTGACC
361 -----+-----+-----+-----+-----+-----+ 420
CTCCTCCGGGTGTAGTTTCGCCCCGGTCTTGGGTGCCACCGTCCTCGACCCGACCACTGG

TACCCAGGGCAGAAGGGCCCGGACTCATCCAGAGGGGAAGGAAGGGTCTTCAGGAAGA
421 -----+-----+-----+-----+-----+-----+ 480
ATGGGTCCCGTCTTCCCGGGCCCTGAGTAGGTCTCCCCTTCCTTCCCCAGAAGTCTTCT

CCACGGAGATGCCACAGGCAGAAATTGGCTTCCCATCTGGGAGATAGGTGGGGAGACCCTG
481 -----+-----+-----+-----+-----+-----+ 540
GGTGCCTCTACGGTGTCCGTCTTAACCGAAGGGTAGACCCTCTATCCACCCCTCTGGGAC

GCATTTTGACAGCCAGAACCTGGGGTGCTGAGCAGAATCTTCATGCCTGGCCTGGCCGCC
541 -----+-----+-----+-----+-----+-----+ 600
CGTAAACTGTTCGGTCTTGGACCCACGACTCGTCTTAGAAGTACGGACCGGACCGGCGG

TTCGGAGGGAAGCTGGAGGGTTGGGTGCGAGAGGAGTGGGGTCAGAGCCCCTACATCCGC
601 -----+-----+-----+-----+-----+-----+ 660
AAGCCTCCCTTCGACCTCCCAACCCACGCTCTCCTCACCCAGTCTCGGGGATGTAGGCG

AGGACCCCAAATCGGCTGGGCCCCAAGGCCCGGACTGCGCTCCCCGGTGGCCCCGGCGCG
661 -----+-----+-----+-----+-----+-----+ 720
TCCTGGGGTTTAGCCGACCCGGGGTTCCGGGCCTGACGCGAGGGGCCACCGGGCCGCGG

CCTCCGCGAATGCGTCTGCCCCCTCCCCTGCCCAAGCCCTCTGCCCTCACCCGGGTCCGG
721 -----+-----+-----+-----+-----+-----+ 780
GGAGGCGCTTACGCAGGACGGGGAGGGGACGGGTTCGGGAGACGGGAGTGGGCCCAGGCC
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CGCCGCCCCCGAAGTGGCGGGAACAACCCGAACCCGAACCTTCTGTCTCTCGGGAGCCCCC
781 -----+-----+-----+-----+-----+-----+-----+ 840
GCGGCGGGGGCTTCACCGCCCTTGTGTTGGGCTTGGGCTTGGGAAGACAGGAGCCCTCGGGGG

AGATAAGCGGCTGGGAACCCGCGGGGCGCAGGGGAGGCCCGGCTGTTCCGCCCCGCTAA
841 -----+-----+-----+-----+-----+-----+-----+ 900
TCTATTGCGCGACCTTGGGCGCCCCGGGCGTCCCCTCCGGGCCGACAAGGCGGGCGATT

GTGCATTAGCACAGCTCACCTCCCCCTATCGCGCCTGCCATCGGACGGGCAGTGCCGCGCC
901 -----+-----+-----+-----+-----+-----+-----+ 960
CACGTAATCGTGTGAGTGGAGGGGATAGCGCGGACGGTAGCCTGCCCCGTCACGGCGCGG

CTGCTCTGGGGCCCCCGGAGCGACCACAGCGGAGGCCGGAACGGACTGTCTTTCTGGGG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
GACGAGACCCCGGGGGCCTCGCTGGTGTGCTCCTCCGGCCTTGCTGACAGGAAAGACCCC

CGGGGTGGGGAGGGGGTGTGCTGGAGGGCCCGGTGGCATAGCAACGGACGAGAGAGGCC
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GCCCCACCCCTCCCCACAGCGACCTCCCGGGCCACCGTATCGTTGCCTGCTCTCTCCGG

TGGAGGAGGGGCGGGGAGGGGGAGTTGTGTGGCAGTTCTAAGGGAAGGGTGGGTGCTGGG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
ACCTCCTCCCCGCCCTCCCCCTCAACACACCGTCAAGATTCCCTTCCCACCCACGACCC

ACGGGTGTCCGGGAGGGAGGGGAGCCTGGCGGGTCTGGGGCCTCGTCGCGGAGGGCGCT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
TGCCACAGGCCCTCCCTCCCTCGGACCGCCCCAGACCCCGGAGCAGCGCCTCCCGCA

GCGAGGGGGAACTGGGGAAAGGGCCTAATTCCCCAGTCTCCACCTCGAATCAGGAAAGA
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
CGCTCCCCCTTTGACCCCTTTCCCGGATTAAGGGGTGAGAGGTGGAGCTTAGTCCCTTCT

GAAGGGGCGGGCTGCTGGGCAAAAGAGGTGAATGGCTGCGGGGGCTGGAGAAGAGAGAT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
CTTCCCCGCGCGACGACCGTTTCTCACTTACCGACGCCCCCGACCTCTTCTCTCTA

GGGAGGGGCGGCGCGGGGGTGGAGGGGTCTAAAGATTGTGGGGGTGAGGAACTGAGG
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
CCCTCCCCGGCGCGCGCCCCACTCCCCAGATTCTAACACCCCCACTCCTTGACTCC

GTGGGGGGCGCCCAGAGGCGGGACTCGGGGCGGGGCAGGCGAGGCGGAGGGCGAGGGCTG
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
CACCCCCGCGGGTCTCCGCCCTGAGCCCCGCCCCGTCCGCTCCGCCTCCCGCTCCCGAC

CGGGAGCAAGTACGAGCCGGGGGTGTGGGGGACGATTGCCGCTGCAGCCGCCGCCCCAC
1441 -----+-----+-----+-----+-----+-----+-----+ 1500
GCCCTCGTTTCATGCCTCGGCCCCCACACCCCTGCTAACGGCGACGTCGGCGGCGGGGTG

TCACCTCCGGTGTGTCTGCAGCCCGGACACTAAGGGAGATGGATGAATGGGTGGGGAGGA
1501 -----+-----+-----+-----+-----+-----+-----+ 1560
AGTGGAGGCCACACAGACGTCGGGCCTGTGATTCCCTCTACCTACTTACCCACCCCTCCT

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TGCGGCGCACATGGCCCCGGGCGGCTCGGCGGTCTAGCTGCCGCCCCACAGCGGACCGGT
1561 -----+-----+-----+-----+-----+-----+-----+ 1620
ACGCCGCGTGTACCGGGGCCCCCGGAGCCGCCAGTCGACGGCGGGGGTGTGCCTGGCCA

CGGGGCGGGGTCTGGGCGGTAGAAAAAGGGCCGCGAGGCGAGCGGGGCACTGGGCGGAC
1621 -----+-----+-----+-----+-----+-----+-----+ 1680
GCCCCGCCCCCAGCCCGCATCTTTTTTCCGCGCTCCGCTCGCCCCGTGACCCGCCTG

CGCGGCGGCAGCATGAGCGGCGCAGACCGTAGCCCCAATGCGGGCGCAGCCCCTGACTCG
1681 -----+-----+-----+-----+-----+-----+-----+ 1740
GCGCCGCGCTCGTACTCGCCGCGTCTGGCATCGGGGTACGCCCCGCTCGGGGACTGAGC

M S G A D R S P N A G A A P D S -

GCCCCGGGCCAGGCGGCGGTGGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCCTACCTC
1741 -----+-----+-----+-----+-----+-----+-----+ 1800
CGGGGCCCCGGTCCGCCGCCACCGAAGCCGGATGGTCGCGAAGCTCGGCGCGCGGATGGAG

A P G Q A A V A S A Y Q R F E P R A Y L -

CGCAACAACCTACGCGCCCCCTCGCGGGGACCTGTGCAACCCGAAGGGCGTCGGGCCGTGG
1801 -----+-----+-----+-----+-----+-----+-----+ 1860
GCGTTGTTGATGCGCGGGGGAGCGCCCCCTGGACACGTTGGGCTTCCGCGAGCCCGGCACC

R N N Y A P P R G D L C N P N G V G P W -

AAGCTGCGCTGCTTGGCGCAGACCTTCGCCACCGGTGAGCGGGGAAACTGAGGCACGAG
1861 -----+-----+-----+-----+-----+-----+-----+ 1920
TTCGACGCGACGAACCGGTCTGGAAGCGGTGGCACTCGCCCCCTTTGACTCCGTGCTC

K L R C L A Q T F A T G (SEQ ID NO:3)

GGACAAGAGGTCTGTCGGGGAGTGAAAGCAGGCGCAGGGAAAATAAAAAAGAAGGAAAGGGAG
1921 -----+-----+-----+-----+-----+-----+-----+ 1980
CCTGTTCTCCAGCAGCCCCCTCACTTTCGTCCGCGTCCCTTTATTTTCTTCCCTTCCCTC

ACAGACCAGGCGCCTAACAGATGGGGACCAAGAAACAAGAGATAGCTGAGAGGTGCAAAC
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
TGTCTGGTCCGCGGATTGTCTACCCCTGGTTCTTTGTTCTCTATCGACTCTCCACGTTTG

AGAAGAGAAAAAGGAGCAACATCCCTTAGGAGAGGGGGCAGAGGAGAGAGAGGTGGAGAGA
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
TCTTCTCTTTTTCCTCGTTGTAGGGAATCCTCTCCCCGTCTCCTCTCTCTCCACCTCTCT

GGGGGCGGAGAGTGCTCAGAATTGAGAGCTAAGGTGGGGGATGCAGGACAGACTGAGGTG
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
CCCCGCTCTCACGAGTCTTAACCTCTCGATTCCACCCCTACGTCTGTCTGACTCCAC

GAGATGCATAGGAGGAAATGGAGGCAGATGTGGGACAGGGGTGAGAACTCCAGGATTTCT
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
CTCTACGTATCCTCCTTTACCTCCGTCTACACCCTGTCCCCACTCTTTGAGGTCCATAAG

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CTCGCTGAGCCTGGCTGGTAGGTATAGTTGTTTCTTTCTTTTCTTTATTTTATTTTCA
2221 -----+-----+-----+-----+-----+-----+ 2280
GAGCGACTCGGACCGACCATCCATATCAACAAAAGAAAGAAAAAGAAATAAAATAAAAGT

TTTATTTACTTATTTTATTTTATTTTATTTTGTTTTGAGACGGAGTTTCGCTCTTGTTGCCCC
2281 -----+-----+-----+-----+-----+-----+ 2340
AAATAAAATGAATAAAAAATAAAAAATAAACAAAACTCTGCCTCAAAGCGAGAACACGGGT

GGCTGGAGTACAATGGCGCCATCTCGGCTCACTGCAACCTCCGCTCCCCGGGTTCAAGC
2341 -----+-----+-----+-----+-----+-----+ 2400
CCGACCTCATGTTACCGCGGTAGAGCCGAGTGACGTTGGAGGCGGAGGGGCCCAAGTTCG

GATTCTCTTGCCCTCAGCTTCCCTAGTAGCTGGGATTACAGGCATGCGCCCCCATGCCTGG
2401 -----+-----+-----+-----+-----+-----+ 2460
CTAAGAGAACGGAGTCGAAGGGATCATCGACCCTAATGTCCGTACGCGGGGGTACGGACC

CTAATTTATTTGTATTTTATTTAGTAGAGACGGGACTTCTCCATGTTGGTCAAGCTGGTCTCG
2461 -----+-----+-----+-----+-----+-----+ 2520
GATTAAATAAACATAAAAAATCATCTCTGCCTGAAGAGGTACAACCAGTCCGACCAGAGC

AACTCCCAACCTTAGGATCCACCCACCCCGGCTCCCAAAGTGCTGGGATTACAGGTGTG
2521 -----+-----+-----+-----+-----+-----+ 2580
TTGAGGGTTGGAATCCTAGGTGGGTGGGGCCGGAGGGTTTCACGACCCTAATGTCCACAC

AGCCACTGCGCCCGGCCAGTAGGTATAGTCTTCTAGATGTGAAACCTGAGTCTCAGAGCG
2581 -----+-----+-----+-----+-----+-----+ 2640
TCGGTGACGCGGGCCGGTCATCCATATCAGAAGATCTACACTTTGGACTCAGAGTCTCGC

GTGAAGTTCCGTTCCGAAGGGCAGCCCATGTTGGAGCTGGGTTCACTCTAACTCTGGGGC
2641 -----+-----+-----+-----+-----+-----+ 2700
CACTTCAAGGGAAGGCTTCCCGTCGGGTACAACCTCGACCCAAGTCAGATTGAGACCCCG

CAATGCTTTTCCAGATGGAGACACATTTGCAGAGGAGAAGGAAGAACTAGAGAGAGGCA
2701 -----+-----+-----+-----+-----+-----+ 2760
GTTACGAAAAAGGTCTACCTCTGTGTAAACGTCTCCTCTTCCTTCTTGATCTCTCTCCGT

GGGAGATGCAGGGGAGGGAAGGGTAAGGAGGCAGGGGCTGCCTGGGCTGGCTGGCACCAG
2761 -----+-----+-----+-----+-----+-----+ 2820
CCCTCTACGTCCCCCTCCCTTCCCATTCCTCCGTCCCCGACGGACCCGACCGACCGTGGTC

GACCCCTCTTCTCTGCCCTGCCCAGGTGAAGTGTCGGGACGCACCCCTCATCGACATTGGT
2821 -----+-----+-----+-----+-----+-----+ 2880
CTGGGAGAAGGAGACGGGACGGGTCCACTTCACAGGCCTGCGTGGGAGTAGCTGTAACCA

E V S G R T L I D I G -

TCAGGCCCCACCGTGTAACAGCTGCTCAGTGCCCTGCAGCCACTTTGAGGACATCCCATG
2881 -----+-----+-----+-----+-----+-----+ 2940
AGTCCGGGGTGGCACATGGTTCGACGAGTCACGGACGTCGGTGAAACTCCTGTAGTGGTAC

S G P T V Y Q L L S A C S H F E D I T M -

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Figure 1 – page 5

ACAGATTTCCTGGAGGTCAACCGCCAGGAGCTGGGGCTGGCTGCAGGAGGAGCCGGGG
 2941 -----+-----+-----+-----+-----+-----+ 3000
 TGTCTAAAGGACCTCCAGTTGGCGGTCTCGACCCCGACCGACGTCTCTCGGGCCC
 T D F L E V N R Q E L G R W L Q E E P G -
 GCCTTCAACTGGAGCATGTACAGCCAACATGCCTGCCTCATTGAGGGCAAGGGGTAAGGA
 3001 -----+-----+-----+-----+-----+-----+ 3060
 CGGAAGTTGACCTCGTACATGTCGGTTGTACGGACGGAGTAACTCCCGTTCCCCATTCTT
 A F N W S M Y S Q H A C L I E G K G (SEQ ID NO:4)
 CTGGGGGGTGAGGGTTGGGGAGGAGGCTTCCCATAGAGTGGCTGGTTGGGGCAACAGAGG
 3061 -----+-----+-----+-----+-----+-----+ 3120
 GACCCCCCACTCCCAACCCCTCCTCCGAAGGGTATCTCACCGACCAACCCCGTTGTCTCC
 CCTGAGCGTAGAACAGCCTTGAGCCCTGCCTTGTGCCTCCTGCACAGGGAATGCTGGCAG
 3121 -----+-----+-----+-----+-----+-----+ 3180
 GGACTCGCATCTTGTTCGGAACTCGGGACGGAACACGGAGGACGTGTCCCTTACGACCGTC
 E C W Q -
 GATAAGGAGCGCCAGCTGCGAGCCAGGGTGAAACGGGTCCTGCCCATCGACGTGCACCAG
 3181 -----+-----+-----+-----+-----+-----+ 3240
 CTATTCTCTCGCGGTTCGACGCTCGGTCCCACTTGGCCAGGACGGGTAGCTGCACGTGGTC
 D K E R Q L R A R V K R V L P I D V H Q -
 CCCCAGCCCCTGGGTGCTGGGAGCCCAGCTCCCCTGCCTGCTGACGCCCTGGTCTCTGCC
 3241 -----+-----+-----+-----+-----+-----+ 3300
 GGGGTCTGGGGACCCACGACCCCTCGGGTCGAGGGGACGGACGACTGCGGGACCAGAGACGG
 P Q P L G A G S P A P L P A D A L V S A -
 TTCTGCTTGGAGGCTGTGAGCCCAGATCTTGCCAGCTTTTACGCGGGCCCTGGACCACATC
 3301 -----+-----+-----+-----+-----+-----+ 3360
 AAGACGAACCTCCGACACTCGGGTCTAGAACGGTCGAAAGTCGCCCCGGGACCTGGTGTAG
 F C L E A V S P D L A S F Q R A L D H I -
 ACCACGCTGCTGAGGCCTGGGGGGCACCTCCTCCTCATCGGGGCCCTGGAGGAGTCGTGG
 3361 -----+-----+-----+-----+-----+-----+ 3420
 TGGTGCGACGACTCCGGACCCCCCTGGAGGAGGAGTAGCCCCGGGACCTCCTCAGCACC
 T T L L R P G G H L L L I G A L E E S W -
 TACCTGGCTGGGGAGGCCAGGCTGACGGTGGTGCCAGTGTCTGAGGAGGAGGTGAGGGAG
 3421 -----+-----+-----+-----+-----+-----+ 3480
 ATGGACCGACCCCTCCGGTCCGACTGCCACCACGGTCACAGACTCCTCCTCCACTCCCTC
 Y L A G E A R L T V V P V S E E E V R E -

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GCCCTGGTGCGTAGTGGCTACAAGGTCCGGGACCTCCGCACCTATATCATGCCTGCCCAC
3481 -----+-----+-----+-----+-----+ 3540
CGGGACCACGCATCACCGATGTTCCAGGCCCTGGAGGCGTGGATATAGTACGGACGGGTG

A L V R S G Y K V R D L R T Y I M P A H -

CTTCAGACAGGCGTAGATGATGTCAAGGGCGTCTTCTTCGCCTGGGCTCAGAAGGTTGGG
3541 -----+-----+-----+-----+-----+ 3600
GAAGTCTGTCCGCATCTACTACAGTTCCCGCAGAAGAAGCGGACCCGAGTCTTCCAACCC

L Q T G V D D V K G V F F A W A Q K V G -

CTGTGAGGGCTGTACCTGGTGCCCTGTGGCCCCCACCACCTGGATTCCCTGTTCTTTGA
3601 -----+-----+-----+-----+-----+ 3660
GACACTCCCGACATGGACCACGGGACACCGGGGGTGGGTGGACCTAAGGGACAAGAACT

L * (SEQ ID NO:5)

AGTGGCACCTAATAAAGAAATAATACCCTGCCGCTGCGGTCAGTGCTGTGTGTGGCTCTC
3661 -----+-----+-----+-----+-----+ 3720
TCACCGTGGATTATTTCTTTATTATGGGACCGCGACGCCAGTCACGACACACACCGAGAG

CTGGGAAGCAGCAAGGGCCCAGAGATCTGAGTGTCCGGGTAGGGGAGACATTACCCCTAG
3721 -----+-----+-----+-----+-----+ 3780
GACCCCTTCGTCGTTCCCGGGTCTCTAGACTCACAGGCCCATCCCTCTGTAAGTGGGATC

GCTTTTTTTTCCAGAAGCTT (SEQ ID NO:1)
3781 -----+----- 3799
CGAAAAAAAGGTCTTCGAA (SEQ ID NO:2)
```

Figure 2A – page 1

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GGCAGCATGAGCGGCGCAGACCGTAGCCCCAATGCGGGCGCAGCCCCTGACTCGGCCCCG
1  -----+-----+-----+-----+-----+-----+ 60
CCGTCGTACTCGCCGCGTCTGGCATCGGGGTACGCCCCGCGTCGGGACTGAGCCGGGGC

      M  S  G  A  D  R  S  P  N  A  G  A  A  P  D  S  A  P  -

GGCCAGGCGGCGGTGGCTTCGGCCTACCAGCGCTTCGAGCCGCGCGCTACCTCCGCAAC
61  -----+-----+-----+-----+-----+-----+ 120
CCGGTCCGCCGCCACCGAAGCCGGATGGTCGCGAAGCTCGGCGCGCGGATGGAGGCGTTG

      G  Q  A  A  V  A  S  A  Y  Q  R  F  E  P  R  A  Y  L  R  N  -

AACTACGCGCCCCCTCGCGGGGACCTGTGCAACCCGAACCGGCGTCGGGCCGTGGAAGCTG
121 -----+-----+-----+-----+-----+-----+ 180
TTGATGCGCGGGGAGCGCCCCCTGGACACGTTGGGCTTGCCGCAGCCCGGCACCTTCGAC

      N  Y  A  P  P  R  G  D  L  C  N  P  N  G  V  G  P  W  K  L  -

CGCTGCTTGGCGCAGACCTTCGCCACCGGTGAAGTGTCGGACGCACCCTCATCGACATT
181 -----+-----+-----+-----+-----+-----+ 240
GCGACGAACCGCGTCTGGAAGCGGTGGCCACTTCACAGGCCTGCGTGGGAGTAGCTGTAA

      R  C  L  A  Q  T  F  A  T  G  E  V  S  G  R  T  L  I  D  I  -

GGTTCAGGCCCCACCGTGTACCAGTGCTCAGTGCCTGCAGCCACTTTGAGGACATCACC
241 -----+-----+-----+-----+-----+-----+ 300
CCAAGTCCGGGGTGGCACATGGTCGACGAGTCACGGACGTCGGTGAAACTCCTGTAGTGG

      G  S  G  P  T  V  Y  Q  L  L  S  A  C  S  H  F  E  D  I  T  -

ATGACAGATTTCTTGGAGGTCAACCGCCAGGAGCTGGGGCGCTGGCTGCAGGAGGAGCCG
301 -----+-----+-----+-----+-----+-----+ 360
TACTGTCTAAAGGACCTCCAGTTGGCGGTCTCGACCCCSCGACCGACGTCCTCCTCGGC

      M  T  D  F  L  E  V  N  R  Q  E  L  G  R  W  L  Q  E  E  P  -

GGGGCCTTCAACTGGAGCATGTACAGCCAACATGCCTGCCTCATTGAGGGCAAGGGGAA
361 -----+-----+-----+-----+-----+-----+ 420
CCCCGGAAGTTGACCTCGTACATGTCGGTTGTACGGACGGAGTAACTCCCGTTCCCCCTT

      G  A  F  N  W  S  M  Y  S  Q  H  A  C  L  I  E  G  K  G  E  -

TGCTGGCAGGATAAGGAGCGCCAGCTGCGAGCCAGGGTGAAACGGGTCCTGCCCATCGAC
421 -----+-----+-----+-----+-----+-----+ 480
ACGACCGTCCTATTCCTCGCGGTGCGACGCTCGGTCCCACTTTGCCAGGACGGGTAGCTG

      C  W  Q  D  K  E  R  Q  L  R  A  R  V  K  R  V  L  P  I  D  -

GTGCACCAGCCCCAGCCCCCTGGGTGCTGGGAGCCCAGCTCCCCTGCCTGCTGACGCCCTG
481 -----+-----+-----+-----+-----+-----+ 540
CACGTGGTTCGGGGTCGGGGACCCACGACCCTCGGGTCGAGGGGACGGACGACTGCGGGAC

      V  H  Q  P  Q  P  L  G  A  G  S  P  A  P  L  P  A  D  A  L  -

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Figure 2A – page 2

GTCTCTGCCTTCTGCTTGGAGGCTGTGAGCCCAGATCTTGCCAGCTTTCAGCGGGCCCTG
541 -----+-----+-----+-----+-----+-----+ 600
CAGAGACGGAAGACGAACCTCCGACACTCGGGTCTAGAACGGTCGAAAGTCGCCCCGGGAC
V S A F C L E A V S P D L A S F Q R A L -
GACCACATCACACGCTGCTGAGGCCTGGGGGGCACCTCCTCCTCATCGGGGCCCTGGAG
601 -----+-----+-----+-----+-----+-----+ 660
CTGGTGTAGTGGTGCACGACTCCGACCCCCCGTGGAGGAGGAGTAGCCCCGGGACCTC
D H I T T L L R P G G H L L L I G A L E -
GAGTCGTGGTACCTGGCTGGGGAGGCCAGGCTGACGGTGGTGCCAGTGTCTGAGGAGGAG
661 -----+-----+-----+-----+-----+-----+ 720
CTCAGCACCATGGACCGACCCCTCCGGTCCGACTGCCACCACGGTCACAGACTCCTCCTC
E S W Y L A G E A R L T V V P V S E E E -
GTGAGGGAGGCCCTGGTGCCTAGTGGCTACAAGGTCCGGGACCTCCGCACCTATATCATG
721 -----+-----+-----+-----+-----+-----+ 780
CACTCCCTCCGGGACCACGCATCACCGATGTTCCAGGCCCTGGAGGCGTGGATATAGTAC
V R E A L V R S G Y K V R D L R T Y I M -
CCTGCCCACCTTCAGACAGGCGTAGATGATGTCAAGGGCGTCTTCTTCGCCTGGGCTCAG
781 -----+-----+-----+-----+-----+-----+ 840
GGACGGGTGGAAGTCTGTCCGCATCTACTACAGTTCCCGCAGAAGAAGCGGACCCGAGTC
P A H L Q T G V D D V K G V F F A W A Q -
AAGGTTGGGCTGTGAGGGCTGTACCTGGTGCCTGTGGCCCCCACCACCTGGATTCCCT
841 -----+-----+-----+-----+-----+-----+ 900
TTCCAACCCGACACTCCCGACATGGACCACGGGACACCGGGGTGGGTGGACCTAAGGGA
K V G L * (SEQ ID NO:8)
GTTCTTTGAAGTGGCACCTAATAAAGAAATAATACC (SEQ ID NO:6)
901 -----+-----+-----+-----+-----+ 936
CAAGAACTTCACCGTGGATTATTTCTTTATTATGG (SEQ ID NO:7)

Figure 2B

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MSGADRSPNAGAAPDSAPGQAAVASAYQRFEPRAYLRNNYAPPRGDLCPNGVGPWKLRC
1  -----+-----+-----+-----+-----+-----+ 60

LAQTFATGEVSGRTLIDIGSGPTVYQLLSACSHFEDITMTDFLEVNRQELGRWLQEEPGA
61 -----+-----+-----+-----+-----+-----+ 120

FNWSMYSQHACLIEGKGECWQDKERQLRARVKRVLPIDVHQPPQPLGAGSPAPLPADALVS
121 -----+-----+-----+-----+-----+-----+ 180

AFCLEAVSPDLASFQRALDHITLLRPGGHLLLIGALEESWYLAGEARLTVVPVSEEEVR
181 -----+-----+-----+-----+-----+-----+ 240

EALVRSGYKVRDLRTYIMPAHLQTGVDDVKGVFFAWAQKVGL (SEQ ID NO:8)
241 -----+-----+-----+-----+-----+--- 282
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Figure 3